

=====

Sequence Listing could not be accepted due to errors.  
See attached Validation Report.  
If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Jun 04 19:15:40 EDT 2007

=====

\*\*\*\*\*

Reviewer Comments:

<110> ARES TRADING S.A.  
<110> FAGAN, Richard Joseph  
<110> DAVIDS, Andrew Robert  
<110> PHELPS, Christopher Benjamin  
<110> POWER, Christine  
<110> BOSCHERT, Ursula  
<110> CHVATCHKO, Yolande

Per 1.823 of the Sequence Rules, the <110> numeric identifier is only shown on the first applicant's line; please delete the additional <110>'s.

<140> PCT/GB2004/004772  
<141> 2004-11-12

Please change the <140> to <150> and the <141> to <151>, since these are prior application data. They are not the current application number and current filing date.

\*\*\*\*\*

Application No: 10579113 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2007-05-22 13:27:47.914  
**Finished:** 2007-05-22 13:27:48.874  
**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 960 ms  
**Total Warnings:** 0  
**Total Errors:** 7  
**No. of SeqIDs Defined:** 31  
**Actual SeqID Count:** 31

Error code	Error Description
E 249	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
E 249	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
E 249	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
E 249	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
E 249	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
E 249	Order Sequence Error <110> -> <110>; Expected Mandatory Tag: <120> in Header
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> ARES TRADING S.A.  
<110> FAGAN, Richard Joseph  
<110> DAVIDS, Andrew Robert  
<110> PHELPS, Christopher Benjamin  
<110> POWER, Christine  
<110> BOSCHERT, Ursula  
<110> CHVATCHKO, Yolande

<120> CYTOKINE AGONIST MOLECULES

<130> P035815WO

<140> PCT/GB2004/004772  
<141> 2004-11-12

<150> GB0326393.6  
<151> 2003-11-12

<160> 31

<170> SeqWin99, version 1.02

<210> 1  
<211> 85  
<212> DNA  
<213> Homo sapiens

<400> 1  
atgaagagag aaaggggagc cctgtccaga gcctccaggg ccctgacgcct tgctcccttt 60  
gtctaccttc ttctgatcca gacag 85

<210> 2  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Lys Arg Glu Arg Gly Ala Leu Ser Arg Ala Ser Arg Ala Leu Arg  
1 5 10 15

Leu Ala Pro Phe Val Tyr Leu Leu Leu Ile Gln Thr Asp  
20 25

<210> 3  
<211> 342  
<212> DNA  
<213> Homo sapiens

<400> 3  
accccttgg a ggggtgaac atcaccagcc ccgtgcgcct gatccatggc accgtgggaa 60  
agtccggctct gctttctgtg cagtacagca gtaccagcag cgacaggcct gtagtgaagt 120  
ggcagctgaa gcgggacaag ccagtgaccg tggtgagtc cattggcaca gaggtcatcg 180  
gcacccttgcg gcctgactat cgagaccgta tccgacttt tgaaaatggc tccctgcttc 240  
tcagcgacct gcagctggcc gatgagggca cctatgaggt cgagatctcc atcaccgacg 300  
acacccatcac tggggagaag accatcaacc ttactgtaga tg 342

<210> 4  
<211> 114  
<212> PRT  
<213> Homo sapiens

<400> 4  
Pro Leu Glu Gly Val Asn Ile Thr Ser Pro Val Arg Leu Ile His Gly  
1 5 10 15

Thr Val Gly Lys Ser Ala Leu Leu Ser Val Gln Tyr Ser Ser Thr Ser  
20 25 30

Ser Asp Arg Pro Val Val Lys Trp Gln Leu Lys Arg Asp Lys Pro Val  
35 40 45

Thr Val Val Gln Ser Ile Gly Thr Glu Val Ile Gly Thr Leu Arg Pro  
50 55 60

Asp Tyr Arg Asp Arg Ile Arg Leu Phe Glu Asn Gly Ser Leu Leu Leu  
65 70 75 80

Ser Asp Leu Gln Leu Ala Asp Glu Gly Thr Tyr Glu Val Glu Ile Ser  
85 90 95

Ile Thr Asp Asp Thr Phe Thr Gly Glu Lys Thr Ile Asn Leu Thr Val  
100 105 110

Asp Val

<210> 5  
<211> 282  
<212> DNA  
<213> Homo sapiens

<400> 5  
tgcccatattc gaggccacag gtgttgtgg cttcaaccac tgtgctggag ctcaagcgagg 60  
ccttcacctt gaactgctca catgagaatg gcaccaagcc cagctacacc tggctgaagg 120  
atggcaagcc cctcctcaat gactcgagaa tgctcctgtc ccccgaccaa aagggtgctca 180  
ccatcacccg cgtgctcatg gaggatgacg acctgtacag ctgcattgtg gagaacccca 240  
tcagccaggg ccgcagcctg cctgtcaaga tcaccgtata ca 282

<210> 6  
<211> 94  
<212> PRT  
<213> Homo sapiens

<400> 6  
Pro Ile Ser Arg Pro Gln Val Leu Val Ala Ser Thr Thr Val Leu Glu  
1 5 10 15

Leu Ser Glu Ala Phe Thr Leu Asn Cys Ser His Glu Asn Gly Thr Lys  
20 25 30

Pro Ser Tyr Thr Trp Leu Lys Asp Gly Lys Pro Leu Leu Asn Asp Ser  
35 40 45

Arg Met Leu Leu Ser Pro Asp Gln Lys Val Leu Thr Ile Thr Arg Val  
50 55 60

Leu Met Glu Asp Asp Asp Leu Tyr Ser Cys Met Val Glu Asn Pro Ile  
65 70 75 80

Ser Gln Gly Arg Ser Leu Pro Val Lys Ile Thr Val Tyr Arg  
85 90

<210> 7

<211> 94

<212> DNA

<213> Homo sapiens

<400> 7

gaagaagctc ccttacatc atcttgtcta caggaggcat cttcctcctt gtgaccttgg 60  
tgacagtctg tgcctgctgg aaaccctcca aaag 94

<210> 8

<211> 31

<212> PRT

<213> Homo sapiens

<400> 8

Arg Ser Ser Leu Tyr Ile Ile Leu Ser Thr Gly Gly Ile Phe Leu Leu  
1 5 10 15

Val Thr Leu Val Thr Val Cys Ala Cys Trp Lys Pro Ser Lys Arg  
20 25 30

<210> 9

<211> 74

<212> DNA

<213> Homo sapiens

<400> 9

gaaacagaag aagctagaaa agcaaaactc cctggaatac atggatcaga atgatgaccg 60  
cctgaaacca gaag 74

<210> 10

<211> 25

<212> PRT

<213> Homo sapiens

<400> 10

Lys Gln Lys Lys Leu Glu Lys Gln Asn Ser Leu Glu Tyr Met Asp Gln  
1 5 10 15

Asn Asp Asp Arg Leu Lys Pro Glu Ala  
20 25

<210> 11

<211> 71

<212> DNA

<213> Homo sapiens

<400> 11  
cagacaccct ccctcgaagt ggtgagcagg aacggaagaa ccccatggca ctctatatcc 60  
tgaaggacaa g 71

<210> 12  
<211> 23  
<212> PRT  
<213> Homo sapiens

<400> 12  
Asp Thr Leu Pro Arg Ser Gly Glu Gln Glu Arg Lys Asn Pro Met Ala  
1 5 10 15

Leu Tyr Ile Leu Lys Asp Lys  
20

<210> 13  
<211> 303  
<212> DNA  
<213> Homo sapiens

<400> 13  
gactccccgg agaccgagga gaaccgggcc ccggagcctc gaagcgcgac ggagccggc 60  
ccgccccggct actccgtgtc tcccggcgtg cccggccgct cgccggggct gcccatccgc 120  
tctgcccccc gctaccccgcg ctccccagcg cgctccccag ccaccggccg gacacactcg 180  
tcgcccccca gggcccccgag ctgcggccggc cgctcgcgca ggcgcctcgcg cacactgcgg 240  
actgcggccg tgacacataat ccgcgagcaa gacgaggccg gcccggtgga gatcagcgcc 300  
tga 303

<210> 14  
<211> 100  
<212> PRT  
<213> Homo sapiens

<400> 14  
Asp Ser Pro Glu Thr Glu Glu Asn Pro Ala Pro Glu Pro Arg Ser Ala  
1 5 10 15

Thr Glu Pro Gly Pro Pro Gly Tyr Ser Val Ser Pro Ala Val Pro Gly  
20 25 30

Arg Ser Pro Gly Leu Pro Ile Arg Ser Ala Arg Arg Tyr Pro Arg Ser  
35 40 45

Pro Ala Arg Ser Pro Ala Thr Gly Arg Thr His Ser Ser Pro Pro Arg  
50 55 60

Ala Pro Ser Ser Pro Gly Arg Ser Arg Ser Ala Ser Arg Thr Leu Arg  
65 70 75 80

Thr Ala Gly Val His Ile Ile Arg Glu Gln Asp Glu Ala Gly Pro Val  
85 90 95

Glu Ile Ser Ala  
100

<210> 15

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 15

atgaagagag aaagggggagc cctgtccaga gcctccaggg ccctgcgcct tgctccttt 60  
gtctaccttc ttctgatcca gacagacccc ctggaggggg tgaacatcac cagccccgtg 120  
cgcctgatcc atggcaccgt ggggaagtcg gctctgctt ctgtgcagta cagcagtacc 180  
agcagcgaca ggcctgttagt gaagtggcag ctgaagcggg acaagccagt gaccgtggtg 240  
cagtcattg gcacagaggt catcggcacc ctgcggcctg actatcgaga ccgtatccga 300  
ctcttgaaa atggctccct gcttctcagc gacctgcagc tggccgatga gggcacctat 360  
gaggtcgaga tctccatcac cgacgacacc ttcaactgggg agaagaccat caaccttact 420  
gtagatgtgc ccatttcgag gccacaggtg ttgggtggctt caaccactgt gctggagctc 480  
agcgaggcct tcaccttgaa ctgctcacat gagaatggca ccaagcccag ctacacctgg 540  
ctgaaggatg gcaagccct cctcaatgac tcgagaatgc tcctgtcccc cgacaaaag 600  
gtgctcacca tcaccgcgt gctcatggag gatgacgacc tgtacagctg catgggtggag 660  
aacccatca gccagggccg cagcctgcct gtcaagatca ccgtatacag aagaagctcc 720  
ctttacatca tcttgtctac aggaggcatc ttccctccttg tgaccttggt gacagtctgt 780  
gcctgctgga aaccctccaa aaggaaacag aagaagctag aaaagcaaaa ctccctggaa 840  
tacatggatc agaatgatga ccgcctgaaa ccagaagcag acaccctccc tcgaagtgg 900  
gagcaggaac ggaagaaccc catggcactc tatatcctga aggacaagga ctcccccggag 960  
accgaggaga acccgccccc ggagcctcga agcgcgacgg agcccgcccc gcccggctac 1020  
tccgtgtctc ccgcctgccc cggccgcgtcg ccggggctgc ccatccgcctc tgcccggccgc 1080  
tacccgcgtc ccccaagcgcg cttccctcagcc accggccgga cacactcgtc gccgcccagg 1140  
gccccgagct cgcccgccg ctcgcgcagc gcctcgcgca cactgcggac tgccggcgtg 1200  
cacataatcc gcgagcaaga cgaggccggc ccgggtggaga tcagcgcctg a 1251

<210> 16

<211> 416

<212> PRT

<213> Homo sapiens

<400> 16

Met Lys Arg Glu Arg Gly Ala Leu Ser Arg Ala Ser Arg Ala Leu Arg

1 5 10 15

Leu Ala Pro Phe Val Tyr Leu Leu Ile Gln Thr Asp Pro Leu Glu

20 25 30

Gly Val Asn Ile Thr Ser Pro Val Arg Leu Ile His Gly Thr Val Gly

35 40 45

Lys Ser Ala Leu Leu Ser Val Gln Tyr Ser Ser Thr Ser Asp Arg

50 55 60

Pro Val Val Lys Trp Gln Leu Lys Arg Asp Lys Pro Val Thr Val Val

65 70 75 80

Gln Ser Ile Gly Thr Glu Val Ile Gly Thr Leu Arg Pro Asp Tyr Arg

85 90 95

Asp Arg Ile Arg Leu Phe Glu Asn Gly Ser Leu Leu Leu Ser Asp Leu

100 105 110

Gln Leu Ala Asp Glu Gly Thr Tyr Glu Val Glu Ile Ser Ile Thr Asp

115 120 125

Asp Thr Phe Thr Gly Glu Lys Thr Ile Asn Leu Thr Val Asp Val Pro  
130 135 140

Ile Ser Arg Pro Gln Val Leu Val Ala Ser Thr Thr Val Leu Glu Leu  
145 150 155 160

Ser Glu Ala Phe Thr Leu Asn Cys Ser His Glu Asn Gly Thr Lys Pro  
165 170 175

Ser Tyr Thr Trp Leu Lys Asp Gly Lys Pro Leu Leu Asn Asp Ser Arg  
180 185 190

Met Leu Leu Ser Pro Asp Gln Lys Val Leu Thr Ile Thr Arg Val Leu  
195 200 205

Met Glu Asp Asp Asp Leu Tyr Ser Cys Met Val Glu Asn Pro Ile Ser  
210 215 220

Gln Gly Arg Ser Leu Pro Val Lys Ile Thr Val Tyr Arg Arg Ser Ser  
225 230 235 240

Leu Tyr Ile Ile Leu Ser Thr Gly Gly Ile Phe Leu Leu Val Thr Leu  
245 250 255

Val Thr Val Cys Ala Cys Trp Lys Pro Ser Lys Arg Lys Gln Lys Lys  
260 265 270

Leu Glu Lys Gln Asn Ser Leu Glu Tyr Met Asp Gln Asn Asp Asp Arg  
275 280 285

Leu Lys Pro Glu Ala Asp Thr Leu Pro Arg Ser Gly Glu Gln Glu Arg  
290 295 300

Lys Asn Pro Met Ala Leu Tyr Ile Leu Lys Asp Lys Asp Ser Pro Glu  
305 310 315 320

Thr Glu Glu Asn Pro Ala Pro Glu Pro Arg Ser Ala Thr Glu Pro Gly  
325 330 335

Pro Pro Gly Tyr Ser Val Ser Pro Ala Val Pro Gly Arg Ser Pro Gly  
340 345 350

Leu Pro Ile Arg Ser Ala Arg Arg Tyr Pro Arg Ser Pro Ala Arg Ser  
355 360 365

Pro Ala Thr Gly Arg Thr His Ser Ser Pro Pro Arg Ala Pro Ser Ser  
370 375 380

Pro Gly Arg Ser Arg Ser Ala Ser Arg Thr Leu Arg Thr Ala Gly Val  
385 390 395 400

His Ile Ile Arg Glu Gln Asp Glu Ala Gly Pro Val Glu Ile Ser Ala  
405 410 415

<212> DNA

<213> Mus musculus

<400> 17

atgaagagag aaaggggagc cctgtcaaga gcctccaggg ctctgcgcct ctctcccttt 60  
gtctacctgc ttctcatcca gccagtcccc ctggaggggg tgaacatcac cagcccagta 120  
cgtctgatcc acggcacagt ggggaagtcg gccctgctt ccgtgcagta cagtagcacc 180  
agcagcgaca agcccggtggt gaagtggcag ctgaagcgtg acaagccagt gaccgtggtg 240  
cagtctatacg gcacagaggt cattggcact ctgcggcctg actatcgaga ccgtatccgg 300  
ctcttgaaa atggctcctt gcttctcagc gacctgcagc tggcggatga gggAACCTAT 360  
gaagtggaga tttccatcac tgacgacacc ttcaccgggg agaagaccat caacctcacc 420  
gtggatgtgc ccatttcaag gccgcaggta ttagtggctt caaccactgt gctggagctc 480  
agtgaggcct tcaccctcaa ctgctcccat gagaatggca ccaagcctag ctacacgtgg 540  
ctgaaggatg gcaaaccct cctcaatgac tcccgaatgc tcctgtcccc tgaccaaaag 600  
gtgctcacca tcacccgagt actcatggaa gatgacgacc tgtacagctg tgtggggag 660  
aacccatca gccaggtccg cagcctgcct gtcaagatca ctgtgtatag aagaagctcc 720  
ctctatatac tcttgtctac aggaggcatc ttcctccttg tgaccctggg gacagttgt 780  
gcctgctgga aaccctcaa aaagtctagg aagaagagga agttggagaa gcaaaactcc 840  
ttggaataca tggatcagaa tcatgaccgc ctaaaatcag aagcagatac cctaccgg 900  
agtggagaac aggagcggaa gaacccaatg gcactctata tcctgaagga taaggattcc 960  
tcagagccag atgaaaaccc tgctacagag ccacggagca ccacagaacc cggccccct 1020  
ggctactccg tgtcgccggc cgtgccccggc cgctctccgg ggcttcccat ccgctcagcc 1080  
cgccgctacc cgcgctcccc agcacgttcc cctgccactg gccggacgca cacgtcgcca 1140  
ccgcggggccc cgagctcgcc aggccgctcg cgtagcttt cgcgctcaact gcggactgca 1200  
ggcgtgcaga gaatccggga gcaggacgag tcagggcagg tggagatcag tgccctga 1257

<210> 18

<211> 418

<212> PRT

<213> Mus musculus

<400> 18

Met Lys Arg Glu Arg Gly Ala Leu Ser Arg Ala Ser Arg Ala Leu Arg

1 5 10 15

Leu Ser Pro Phe Val Tyr Leu Leu Leu Ile Gln Pro Val Pro Leu Glu

20 25 30

Gly Val Asn Ile Thr Ser Pro Val Arg Leu Ile His Gly Thr Val Gly

35 40 45

Lys Ser Ala Leu Leu Ser Val Gln Tyr Ser Ser Thr Ser Ser Asp Lys

50 55 60

Pro Val Val Lys Trp Gln Leu Lys Arg Asp Lys Pro Val Thr Val Val

65 70 75 80

Gln Ser Ile Gly Thr Glu Val Ile Gly Thr Leu Arg Pro Asp Tyr Arg

85 90 95

Asp Arg Ile Arg Leu Phe Glu Asn Gly Ser Leu Leu Leu Ser Asp Leu

100 105 110

Gln Leu Ala Asp Glu Gly Thr Tyr Glu Val Glu Ile Ser Ile Thr Asp

115 120 125

Asp Thr Phe Thr Gly Glu Lys Thr Ile Asn Leu Thr Val Asp Val Pro

130 135 140  
Ile Ser Arg Pro Gln Val Leu Val Ala Ser Thr Thr Val Leu Glu Leu  
145 150 155 160  
Ser Glu Ala Phe Thr Leu Asn Cys Ser His Glu Asn Gly Thr Lys Pro  
165 170 175  
Ser Tyr Thr Trp Leu Lys Asp Gly Lys Pro Leu Leu Asn Asp Ser Arg  
180 185 190  
Met Leu Leu Ser Pro Asp Gln Lys Val Leu Thr Ile Thr Arg Val Leu  
195 200 205  
Met Glu Asp Asp Asp Leu Tyr Ser Cys Val Val Glu Asn Pro Ile Ser  
210 215 220  
Gln Val Arg Ser Leu Pro Val Lys Ile Thr Val Tyr Arg Arg Ser Ser  
225 230 235 240  
Leu Tyr Ile Ile Leu Ser Thr Gly Gly Ile Phe Leu Leu Val Thr Leu  
245 250 255  
Val Thr Val Cys Ala Cys Trp Lys Pro Ser Lys Lys Ser Arg Lys Lys  
260 265 270  
Arg Lys Leu Glu Lys Gln Asn Ser Leu Glu Tyr Met Asp Gln Asn Asp  
275 280 285  
Asp Arg Leu Lys Ser Glu Ala Asp Thr Leu Pro Arg Ser Gly Glu Gln  
290 295 300  
Glu Arg Lys Asn Pro Met Ala Leu Tyr Ile Leu Lys Asp Lys Asp Ser  
305 310 315 320  
Ser Glu Pro Asp Glu Asn Pro Ala Thr Glu Pro Arg Ser Thr Thr Glu  
325 330 335  
Pro Gly Pro Pro Gly Tyr Ser Val Ser Pro Pro Val Pro Gly Arg Ser  
340 345 350  
Pro Gly Leu Pro Ile Arg Ser Ala Arg Arg Tyr Pro Arg Ser Pro Ala  
355 360 365  
Arg Ser Pro Ala Thr Gly Arg Thr His Thr Ser Pro Pro Arg Ala Pro  
370 375 380  
Ser Ser Pro Gly Arg Ser Arg Ser Ser Arg Ser Leu Arg Thr Ala  
385 390 395 400  
Gly Val Gln Arg Ile Arg Glu Gln Asp Glu Ser Gly Gln Val Glu Ile  
405 410 415  
Ser Ala

<211> 720  
<212> DNA  
<213> Homo sapiens

<400> 19

atgaagagag aaagggggagc cctgtccaga gcctccaggg ccctgcgcct tgctccttt 60  
gtctaccttc ttctgatcca gacagacccc ctggaggggg tgaacatcac cagccccgtg 120  
cgccctgatcc atggcaccgt ggggaagtcg gctctgctt ctgtgcagta cagcagtacc 180  
agcagcgaca ggcctgttagt gaagtggcag ctgaagcggg acaagccagt gaccgtggtg 240  
cagtcattg gcacagaggt catcggcacc ctgcggcctg actatcgaga ccgtatccga 300  
ctcttgaaa atggctccct gcttctcagc gacctgcagc tggccgatga gggcacctat 360  
gaggtcgaga tctccatcac cgacgacacc ttcaactgggg agaagaccat caaccttact 420  
gtagatgtgc ccatttcgag gccacaggtg ttgggtggctt caaccactgt gctggagctc 480  
agcgaggcct tcaccttgaa ctgctcacat gagaatggca ccaagcccag ctacacctgg 540  
ctgaaggatg gcaagccct cctcaatgac tcgagaatgc tcctgtcccc cgacccaaag 600  
gtgctcacca tcaccggcgt gctcatggag gatgacgacc tgtacagctg catgggtggag 660  
aacccatca gccagggccg cagcctgcct gtcaagatca ccgtatacag aagaagctcc 720

<210> 20

<211> 240

<212> PRT

<213> Homo sapiens

<400> 20

Met Lys Arg Glu Arg Gly Ala Leu Ser Arg Ala Ser Arg Ala Leu Arg  
1 5 10 15

Leu Ala Pro Phe Val Tyr Leu Leu Leu Ile Gln Thr Asp Pro Leu Glu  
20 25 30